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(11) Publication number: **0 678 523 A1**

(12)

EUROPEAN PATENT APPLICATION
published in accordance with Art.
158(3) EPC

(21) Application number: 93901547.5

(22) Date of filing: 14.01.93

(86) International application number:
PCT/JP93/00039

(87) International publication number:
WO 94/15969 (21.07.94 94/17)

(51) Int. Cl.⁸: C07K 15/28, C12P 21/08,
C12N 15/13, //A61K39/395,
(C12P21/08, C12R1:91)

(43) Date of publication of application:
25.10.95 Bulletin 95/43

(94) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IE IT LI LU MC
NL PT SE

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(54) RECOMBINANT ANTI-HIV ANTIBODY AND PREPARATION THEREOF.

(57) The invention relates to a gene fragment which codes for the variable regions of an antibody having an activity of neutralizing human immunodeficiency virus (HIV), a novel recombinant anti-HIV antibody expressed by using the above gene, and a process for preparing the same. A mouse-human chimeric antibody and a modified mouse-human antibody, having an activity of neutralizing HIV, are obtained by determining a specific nucleic acid sequence of a gene fragment which codes for the variable regions of the H and L chains of an antibody having an activity of neutralizing HIV and artificially fusing a DNA synthesized on the basis of the determined sequence with a gene which codes for human immunoglobulin. The novel anti-HIV antibody is useful for treating and preventing AIDS.

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Technical Field of the Invention

The present invention relates to a novel recombinant anti-HIV antibody which can be expected to be used for treatment and prevention of AIDS provoked by human immunodeficiency virus (HIV). More specifically, the present invention relates to a recombinant anti-HIV antibody (reshaped antibody and chimeric antibody) having a neutralizing activity against HIV, said antibody being expressed using a genetic recombination technique from a mouse immunoglobulin gene and a human immunoglobulin gene, and a novel process for preparing the same. The present invention further relates to DNA fragments coding for H chain and L chain variable region which can be effectively used for expression of such useful recombinant antibody.

Background Art

Acquired immunodeficiency syndrome (AIDS) is a viral disease caused by human immunodeficiency virus (HIV) belonging to a retrovirus. This disease, since discovery in the United States in 1981, has rapidly been spreading all over the world but an effective vaccine or a method for treating said disease has not yet been established.

Under such circumstances, there are reports on a relevance between the clinics and a neutralizing antibody in a group of thalassemic patients exhibiting HIV positive through transfusion and in a group of children with AIDS or ARC (AIDS related syndrome) [R. Guroff et al., J.Immunol., 138, p3731, (1987); R. Guroff et al., Pediatric Research, inpress]. It is mentioned in both reports that the clinical symptom was mild and benign in such cases where a neutralizing antibody was detectable, whereas it has become malignant in such cases where no neutralizing antibody could be detected. These facts suggest *in vivo* effectiveness of a neutralizing antibody. Therefore, an anti-HIV neutralizing antibody is expected to be usable for prevention of expansion of infection or for exclusion of infected cells, and to show a more enhanced effect when used in combination with anti-viral agents etc. now currently used clinically.

Though it is possible that the anti-HIV neutralizing antibody as mentioned above is directly obtained or prepared from patients with AIDS, this method is expected to bear a number of difficulties such as an ethical problem, availability of materials or a problem of biohazard. In this respect, as an alternative of such a high titer serum, the use of a monoclonal antibody having a neutralizing activity against HIV virus is considered. Although a basic technique for preparation of a monoclonal antibody has already been established in a mouse-type monoclonal antibody, a mouse antibody is hardly applicable to clinical applications in view of side effects (a mouse monoclonal antibody, when administered to humans, is considered to cause side effects such as anaphylactic shock or serum disease as a heterogeneous protein) etc., and hence, the use of a human monoclonal antibody is eventually preferable.

However, preparation of a human monoclonal antibody provokes many problems to be overcome for preparing an antibody having a desired specificity and is actually quite difficult in comparison to preparation of a mouse-type monoclonal antibody. For overcoming such problems, a method for preparing a chimeric monoclonal antibody utilizing a genetic recombination technique has recently been reported wherein the variable region, which characterizes the specificity of an antibody, has an amino acid sequence derived from a mouse antibody and the constant region has an amino acid sequence derived from a human antibody.

Such chimeric monoclonal antibody is obtained by expressing a mouse(V)-human(C) chimeric antibody gene, comprising a variable (V) gene as a material for V region which is cloned from a mouse hybridoma producing a mouse monoclonal antibody and a constant (C) gene as a material for C region which is cloned from a human cell such as a human antibody-producing cell, in an animal cell or a microorganism cell, etc., the desired chimeric monoclonal antibody being present in a culture supernatant. There have been several reports on a chimeric antibody [Japanese Patent First Publication No. 60-155132, Japanese Patent First Publication No. 61-47500] and the present inventors have already successfully prepared a chimeric antibody [Japanese Patent First Publication No. 2-2352]. Moreover, to further this idea of a chimeric antibody, preparation of a reshaped antibody has also been reported [Japanese Patent First Publication No. 62-296890].

Analysis of an immunoglobulin gene has made a rapid progress with a rapid advance of a genetic manipulation technique nowadays. It is well known that an immunoglobulin gene consists of a variable region (V region) gene involved in binding with an antigen and a constant region (C region) gene having a physiological activity concerned with interactions with complement or specific cells, etc. A V region gene is formed by each one gene selected from a group of V gene fragments, a group of D gene fragments (not found in an L chain) and a group of J gene fragments, each selected genes being bound in

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this order Furthermore, the bound gene fragment (V region gene) is further altered by a minute modification with a somatic mutation. That is, a specificity of an antibody is determined by a combination of each of gene fragments in V region gene of H chain and L chain and a somatic mutation [cf. Susumu Tonegawa, Nature, 307, p575 (1983); Tasuku Honjo, Annual Rev. Immunol. 1, p499 (1983)]. Accordingly, for a specific antigen, there seems to be both a combination of a specific VDJ gene fragment of H chain and a specific VJ gene fragment of L chain and a specific somatic mutation. In addition, a combination of these gene fragments or nucleotide or amino acid sequence thereof can hardly be deduced from a structure, nucleotide or amino acid sequence etc. of an antigen but can only be determined by isolating an antibody gene or an antibody protein from cells actually producing an antibody. In this way, a variable region of an antibody molecule has an amino acid sequence varying with every antigen determinant, and a variable region has an amino acid sequence which completely varies with every antigen.

As for a recombinant anti-HIV antibody aimed by the present invention, the present inventors have already published 0.58 recombinant antibody as an anti-HIV neutralizing antibody [Japanese Patent First Publication No. 2-2352], but said recombinant antibody can specifically neutralize HTLV-III_B but not HTLV-III_{MN} which is epidemically prevalent. As mentioned above, for preparation of a recombinant antibody, it is very important to find out a gene coding for an amino acid sequence of a variable region of an antibody molecule having a binding capacity with a desired antigen. Because of difficulty of finding a gene coding for an amino acid sequence of a variable region of an antibody having a neutralizing activity against HIV, especially HTLV-III_{MN}, aimed by the present invention, there is no report of obtention of a recombinant antibody which binds with and substantially neutralizes HTLV-III_{MN}.

Object of the Invention

Under such circumstances, the present inventors have successfully isolated a gene coding for a variable region of a monoclonal antibody having a neutralizing activity against HIV (HTLV-III_{MN}) from cells (hybridomas) producing said antibody. The present inventors have further attempted to make an expression of a mouse-human recombinant antibody using said gene, and as a result, have successfully prepared a recombinant antibody having a neutralizing activity against HIV (HTLV-III_{MN}), and thus the present invention has been completed. That is, the present invention provides for a gene coding for a variable region of an anti-HIV neutralizing antibody which has hitherto never been reported, and provides for a recombinant anti-HIV antibody expressed in a transformed cell by using said gene. An object of the present invention is to make it possible to develop diagnosing, treating and preventing agents for AIDS with decreased side effects comprising said novel anti-HIV recombinant antibody.

Brief Explanation of Drawings

Fig. 1 shows a nucleotide sequence of a DNA fragment of the present invention coding for H chain variable region of anti-HIV neutralizing antibody μ 39.1 shown in Example (3) and an amino acid sequence deduced therefrom.

Fig. 2 shows a nucleotide sequence of a DNA fragment of the present invention coding for L chain variable region of anti-HIV neutralizing antibody μ 39.1 shown in Example (3) and an amino acid sequence deduced therefrom.

Fig. 3 shows a nucleotide sequence of a DNA fragment of the present invention coding for H chain variable region of anti-HIV neutralizing antibody μ 5.5 shown in Example (3) and an amino acid sequence deduced therefrom.

Fig. 4 shows a nucleotide sequence of a DNA fragment of the present invention coding for L chain variable region of anti-HIV neutralizing antibody μ 5.5 shown in Example (3) and an amino acid sequence deduced therefrom.

Fig. 5 shows a structure of anti-HIV chimeric antibody H chain expression plasmids, CH μ 39.1 and CH μ 5.5, constructed in Example (4).

Fig. 6 shows a structure of anti-HIV chimeric antibody L chain expression plasmids, CL μ 39.1 and CL μ 5.5, constructed in Example (4).

Fig. 7 shows anti-HIV activities of anti-HIV chimeric antibody μ 39.1 measured in Example (5) and of anti-HIV reshaped antibody μ 39.1 measured in Example (7).

Fig. 8 shows anti-HIV activities of anti-HIV chimeric antibody μ 5.5 measured in Example (5) and of anti-HIV reshaped antibody μ 5.5 measured in Example (7).

Fig. 9 shows a nucleotide sequence of a DNA fragment coding for an H chain variable region of anti-HIV reshaped antibody μ 39.1 prepared in Example (6) and an amino acid sequence deduced therefrom (the

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underlined sequence shows an amino acid sequence derived from a mouse antibody).

Fig. 10 shows a nucleotide sequence of a DNA fragment coding for an L chain variable region of anti-HIV reshaped antibody μ 39.1 prepared in Example (6) and an amino acid sequence deduced therefrom (the underlined sequence shows an amino acid sequence derived from a mouse antibody).

5 Fig. 11 shows a nucleotide sequence of a DNA fragment coding for an H chain variable region of anti-HIV reshaped antibody μ 5.5 prepared in Example (8) and an amino acid sequence deduced therefrom (the underlined sequence shows an amino acid sequence derived from a mouse antibody).

Fig. 12 shows a nucleotide sequence of a DNA fragment coding for an L chain variable region of anti-HIV reshaped antibody μ 5.5 prepared in Example (6) and an amino acid sequence deduced therefrom (the underlined sequence shows an amino acid sequence derived from a mouse antibody).

Disclosure of the Invention

Cells producing anti-HIV (HTLV-III_{MN}) mouse monoclonal antibody used in the present invention are prepared by the hitherto established technique for preparing a mouse monoclonal antibody. For example, it can be prepared by immunizing mice with an appropriate immunogen, e.g. a viral particle obtained from HIV (HTLV-III_{MN}) producing cells, or a purified envelope glycoprotein gp120, or a recombinant peptide prepared by using a genetic recombination technique, preferably a recombinant peptide corresponding to gp120 amino acid sequence Nos. 247-370, or a suitable synthetic peptide prepared based on an amino acid sequence of said viral protein, preferably a synthetic peptide corresponding to gp120 amino acid sequence Nos. 303-325, etc., fusing the obtained spleen cells with mouse myeloma cells, selecting from the obtained hybridomas the cells which react with a purified envelope glycoprotein gp120 or the above recombinant peptide or the above synthetic peptide, and culturing said cells. Further, from the thus obtained anti-HIV mouse monoclonal antibody producing cells, the cells producing a monoclonal antibody having a neutralizing activity against HIV are selected. In case of HIV, it is not easy to obtain a monoclonal antibody having such neutralizing activity due to characteristics of its own, but as such a cell line, the present inventors have already successfully established hybridomas μ 39.1 and μ 5.5 cells which produce an antibody having a neutralizing activity against HIV (HTLV-III_{MN}) [Japanese Patent Application No. 2-188300], these cell lines being most preferably used for the present invention.

30 The gene fragment coding for a variable region of the present invention is isolated from the above-mentioned anti-HIV neutralizing monoclonal antibody producing cells and a gene sequence thereof is analyzed. However, as mentioned above, such cells contains a large number of genes consisting of V region in addition to a gene coding for a V region specific for a desired anti-HIV antibody (For example, a group of V gene alone of VH chain which determines a specificity of a mouse antibody includes more than 100 different genes, a group of D gene includes more than 11 genes, and a group of J gene includes 4 genes. Similarly, a group of V gene of V_H chain includes more than about 300 genes, and a group of J gene includes 4 genes), and hence, it is necessary to isolate a gene coding for a V region specific for a desired anti-HIV antibody. A V region gene can be isolated by the conventional gene manipulation technique, including, for example, a method of cloning a V region gene from a chromosomal DNA of the cell by using the conventional method [cf. for example, T. Maniatis "Molecular Cloning" Cold Spring Harbor Lab. (1982)] or a method of synthesizing cDNA from mRNA of the cells using the conventional method [e.g. D.M.Glover ed. "DNA cloning Vol. I" IRL press (1985)] and cloning the V region gene. In either method, there can be utilized, as a probe for cloning a V region gene, a DNA probe etc. synthesized by referring to the nucleotide sequence of a mouse immunoglobulin gene which has already been reported [e.g. Sakano et al., Nature, 286, p676, (1980); E.E.Max et al., J. Biol. Chem., 256, p5116, (1981)]. Cloning with PCR (polymerase chain reaction) can also be conducted [R. Orlandi, et al., Proc. Natl. Acad. Sci. USA, 86, 3833 (1989); W.D.Huse, et al., Science, 246, 1275 (1989)].

The thus cloned V region gene was genetically analyzed by various methods such as a method for preparing a chimeric antibody [Japanese Patent First Publication No. 2-2352] or a method for preparing a reshaped antibody [Japanese Patent First Publication No. 62-296890]. As a result, it was found that the gene fragment of the present invention coding for an anti-HIV antibody V region is characterized by that it contains, as a specific gene sequence, a gene coding for an amino acid of (H-a):

- (a) Lys-Tyr-Gly-Met-Asn
 (b) Trp-Lys-Asn-Thr-Asn-Thr-Gly-Glu-Ser-Thr-His-Val-Glu-Glu-Phe-Lys-Gly
 55 (c) Glu-Tyr-Asp-Tyr-Asp-Gly-Gly-Phe-Ser-Tyr or (H-b):
 (a) Glu-Tyr-Thr-Met-His
 (b) Gly-Ile-Asn-Pro-Asn-Asn-Gly-Asp-Thr-Ser-Tyr-Thr-Gln-Lys-Phe-Lys-Gly

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(c) Pro-Tyr-Tyr-Ala-Tyr-Ala-Ile-Asp-Ser within a gene coding for H chain as a part, and a gene sequence coding for an amino acid of (L-a):

(a) Lys-Ala-Ser-Gln-Asp-Val-Gly-Ala-Asp-Val-Ala

(b) Trp-Ala-Ser-Thr-Arg-His-Thr

5 (c) Gln-Gln-Tyr-Ser-Ser-Phe-Pro-Leu-Thr or (L-b):

(a) Lys-Ala-Ser-Gln-Ser-Val-Asp-Tyr-Asp-Gly-Asp-Ser-Tyr-Met-Asn

(b) Ala-Ala-Ser-Asn-Leu-Glu-Ser

(c) Gln-Gln-Ser-Asn-Glu-Asp-Pro-Trp-Thr

10 within a gene coding for L chain as a part. Each set of these three amino acid sequences contained in H chain and L chain, respectively, are considered to be an important amino acid sequence which determines a binding capacity of an antibody molecule and such amino acid sequences were considered to be closely related to a function of an antibody molecule having a neutralizing activity against HIV. That is, by referring to the results of general analysis of an antibody gene reported by Kabat et al. [Sequences of Proteins of Immunological Interest, 4th. ed. U.S. Department of Health and Human Services (1987)], the above amino acid sequences were found to be a sequence of complementarity determining regions (CDR1 to CDR3) in a variable region which determines an antibody activity of the anti-HIV antibody of the present invention. A gene coding for such variable region of an antibody molecule having an anti-HIV neutralizing activity includes, by way of a preferable example, gene fragments coding for the amino acid sequences as shown in Fig. 1 or Fig. 3 or for the amino acid sequences as shown in Fig. 2 or Fig. 4 for H chain or L chain, respectively. A specific nucleotide sequence of such genes includes, for example, the nucleotide sequences as shown in Fig. 1 or Fig. 3, or Fig. 2 or Fig. 4, for H chain or L chain, respectively.

20 Based on the above nucleotide sequences provided by the present invention, a recombinant antibody having a neutralizing activity against HIV can be prepared. That is, a desired recombinant anti-HIV antibody, i.e. anti-HIV chimeric antibody or anti-HIV reshaped antibody, can be prepared by preparing, as a gene coding for a variable region of such recombinant antibody, synthetic DNAs etc. which are DNA fragments coding for the above amino acid sequences as a complementarity determining region, and fusing said DNAs with a gene coding for a human immunoglobulin. The thus prepared recombinant anti-HIV antibody of the present invention is characterized by that it contains, as a complementarity determining region of H chain variable region, the following sequences (CDR1 to CDR3):

30 (H-A)

CDR1: Lys-Tyr-Gly-Met-Asn

CDR2: Trp-Lys-Asn-Thr-Asn-Thr-Gly-Glu-Ser-Thr-His-Val-Glu-Glu-Phe-Lys-Gly

CDR3: Glu-Tyr-Asp-Tyr-Asp-Gly-Gly-Phe-Ser-Tyr or

(H-B)

35 CDR1: Glu-Tyr-Thr-Met-His

CDR2: Gly-Ile-Asn-Pro-Asn-Asn-Gly-Asp-Thr-Ser-Tyr-Thr-Gln-Lys-Phe-Lys-Gly

CDR3: Pro-Tyr-Tyr-Ala-Tyr-Ala-Ile-Asp-Ser.

The recombinant anti-HIV antibody of the present invention is also characterized by that it contains, as a complementarity determining region of L chain variable region, the following sequences (CDR1 to CDR3):

40 (L-A)

CDR1: Lys-Ala-Ser-Gln-Asp-Val-Gly-Ala-Asp-Val-Ala

CDR2: Trp-Ala-Ser-Thr-Arg-His-Thr

CDR3: Gln-Gln-Tyr-Ser-Ser-Phe-Pro-Leu-Thr or

(L-B):

45 CDR1: Lys-Ala-Ser-Gln-Ser-Val-Asp-Tyr-Asp-Gly-Asp-Ser-Tyr-Met-Asn

CDR2: Ala-Ala-Ser-Asn-Leu-Glu-Ser

CDR3: Gln-Gln-Ser-Asn-Glu-Asp-Pro-Trp-Thr.

50 Furthermore, the present inventors have also found that, in preparing a reshaped antibody, a recombinant antibody which more fully retains an original antibody activity can be obtained by replacing, in addition to complementarity determining regions, a portion of frame (FR) region adjacent to said complementarity determining regions with a mouse-derived sequence rather than by replacing the complementarity determining regions alone with a mouse-derived sequence as hitherto reported.

55 That is, when the above complementarity determining region sequences (H-A) are used as an H chain variable region gene, an anti-HIV reshaped antibody having a more excellent activity can be prepared by preparing an H chain variable region gene wherein one amino acid at the C terminus of FR1 adjacent to the complementarity determining region CDR1 in a variable region is threonine (Thr), a four amino acid sequence at the C terminus of FR2 adjacent to CDR2 is Lys-Trp-Met-Gly, a five amino acid sequence at the N terminus of FR3 adjacent to CDR2 is Arg-Val-Thr-Met-Ser and one amino acid at the C terminus of FR3

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adjacent to CDR3 is arginine (Arg). Similarly, when the above complementarity determining region sequences (H-B) are used as an H chain variable region gene, an anti-HIV reshaped antibody having a more excellent activity can be prepared by preparing an H chain variable region gene wherein one amino acid at the C terminus of FR1 adjacent to the complementarity determining region CDR1 in a variable region is threonine (Thr), a two amino acid sequence at the C terminus of FR2 adjacent to CDR2 is Ile-Gly, a six amino acid sequence at the N terminus of FR3 adjacent to CDR2 is Lys-Ala-Thr-Met-Thr-Val and one amino acid at the C terminus of FR3 adjacent to CDR3 is threonine (Thr). When the above complementarity determining region sequences (L-A) are used as an L chain variable region gene, it is preferable to prepare an L chain variable region gene wherein one amino acid at the C terminus of FR2 adjacent to the complementarity determining region CDR2 in a variable region is serine (Ser).

A nucleotide sequence of the thus prepared gene coding for an H chain variable region of the anti-HIV reshaped antibody of the present invention, and an amino acid sequence deduced therefrom, includes, as a preferable example, the sequences as shown in Fig. 9 or Fig. 11 (wherein the underlined portion shows an amino acid sequence derived from mice). On the other hand, a nucleotide sequence of the gene coding for an L chain variable region of the anti-HIV reshaped antibody of the present invention, and an amino acid sequence deduced therefrom, includes, as a preferable example, the sequences as shown in Fig. 10 or Fig. 12 (wherein the underlined portion shows an amino acid sequence derived from mice).

On the other hand, in preparing an anti-HIV chimeric antibody in accordance with the present invention, a nucleotide sequence of the gene coding for an H chain variable region and an amino acid sequence deduced therefrom includes, as a preferable example, the sequences as shown in Fig. 1 or Fig. 3. A nucleotide sequence of the gene coding for an L chain variable region and an amino acid sequence deduced therefrom includes, as a preferable example, the sequences as shown in Fig. 2 or Fig. 4.

On the other hand, a constant (C) region gene of a human immunoglobulin H chain gene and L chain gene used for preparing the anti-HIV recombinant antibody can be isolated in the same manner, for example, from a human antibody producing cell. Since rearrangement does not occur in a C region gene, a human antibody producing cell is not necessarily used for isolating a human C region gene. The isolation can be conducted in the same way as in the isolation of the mouse V region gene as mentioned above. A C region gene is not limited to γ 1 chain or κ chain but any kind of C region gene such as μ chain, α chain, γ 2 chain, γ 3 chain, γ 4 chain, ϵ chain, or λ chain can be used. However, if a complement activating capacity or an antibody-dependent cellular cytotoxicity is desired, γ 1 chain is preferable.

The anti-HIV recombinant antibody gene, both an H chain gene and an L chain gene, can be constructed basically by combining the above-mentioned two gene fragments (V region gene and C region gene). For example, the construction can be carried out in accordance with the method previously shown by Watanabe et al. [Watanabe et al., Cancer Research, 47, p999-1005, (1987)], or methods outlined by M. Bruggemann [Waldmann H (ed) Monoclonal Antibody Therapy. Prog Allergy. Basel, Karger, 1988, vol 45, pp91] or by S. L. Morrison [Advances in Immunology, 44, 65, (1989)]. A vector system varies depending on a host used for expression such as an animal cell expression system, an E. coli expression system, or an yeast expression system, but the gene of the present invention can be expressed in any of these expression systems. In addition, a gene amplification system such as DHFR may also be used.

The thus prepared recombinant antibody of the present invention was confirmed to have a neutralizing activity against HIV, and hence, the present invention allows for preparation of an anti-HIV recombinant antibody which hitherto has never been prepared. Such anti-HIV recombinant antibody, in the clinic of AIDS, can be a substantially effective treating agent for AIDS. Furthermore, the gene fragments coding for the anti-HIV antibody variable region provided by the present invention disclose a specific amino acid sequence or nucleotide sequence of a variable region of an antibody having a neutralizing activity against HIV and allows for development of a more excellent anti-HIV recombinant antibody molecule through modification or partial replacement of a desired antibody molecule by employing a further advanced genetic recombination technique.

Best Mode for Carrying out the Invention

The present invention is explained in more detail by Examples but it should not be construed to be limited thereto.

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Example

(1) Preparation of anti-HIV mouse monoclonal antibody producing cells

A method for preparing a hybridoma producing an anti-HIV mouse monoclonal antibody is shown hereinbelow. An antigen for immunization included a synthetic peptide corresponding to an amino acid sequence Nos. 303 to 325 of HTLV-IIIMN strain envelope glycoprotein gp120 (SP-1: YNKRKRIHIGPG-
 5 RAFYTTKNIG) and a peptide-KLH (keyhole limpet hemocyanin) conjugate comprising said synthetic peptide bound to KLH, or a viral particle obtained from a culture supernatant of HTLV-IIIMN producing cells
 10 (H9/HTLV-IIIMN) by sucrose density-gradient centrifugation, or gp120 obtained by lysing cells from H9/HTLV-IIIMN culture with 1% TritonX-100 and then purifying by affinity chromatography through ConA-Sephrose 4B column and HIV antibody (IgG)-Sephrose 4B column, or HTLV-IIIMN gp120 V3 domain (amino acid 247-370) β -galactosidase fused protein which is prepared by isolating and amplifying by PCR
 15 method [G. I. LaRosa et al., Science Vol. 249 p832 (1990)] a DNA fragment coding for HTLV-IIIMN gp120 V3 domain (amino acid 247-370) from a high molecular weight DNA (genomic DNA) of H9/HTLV-IIIMN cells and expressing said DNA fragment in E. coli using pUEX2 (manufactured by Amersham) expression vector, or a combination of these antigens. After immunization of BALB/c mice 4 times with these immunogens, spleen cells were taken out and cell-fused with P3X63Ag8-U1X63 mouse myeloma cells [ATCC CRL 1597] using polyethylene glycol (Sigma) and cloning was conducted. A binding activity to the above immunogens
 20 of antibodies in the culture supernatant of the obtained clones was measured by enzyme immunoassay. For the clones deemed to be positive, the results were further confirmed by a Western blotting method and an indirect fluorescence method to establish hybridomas producing anti-HIV monoclonal antibodies, μ 39.1 or μ 5.5 [Japanese Patent Application No. 2-188300, deposit number; μ 39.1 (P-11472), μ 5.5 (BP-3402)]. These antibodies bind to SP-1 peptide and inhibit syncytium formation between HIV-infected cells and uninfected
 25 CD4 positive cells. Furthermore, a neutralizing activity of these antibodies was also confirmed in a viral neutralization test where these antibodies are mixed with HIV virus and cells (H9) are infected with this mixture.

For preparing a V region gene of the anti-HIV recombinant antibody of the present invention as mentioned hereinbelow, the cells producing these anti-HIV mouse monoclonal antibodies having said
 30 neutralizing activity (μ 39.1, μ 5.5 cells) were used.

(2) Isolation of anti-HIV antibody mouse V region gene

The isolation of a mouse immunoglobulin variable (V) region gene was carried out in the following
 35 manner.

A whole RNAs were extracted from μ 39.1 and μ 5.5 cells in accordance with the conventional method [D.M.Glover ed. "DNA cloning Vol. I" IRL press (1985)] and a single-stranded cDNA was synthesized using a cDNA synthesizer System Plus (Amersham). Using this single-stranded cDNA as a template, a polymerase chain reaction (PCR) was conducted using DNA primers which were synthesized based on the
 40 nucleotide sequences of V region and J region as classified by Kabat et al. [Sequences of Proteins of Immunological Interest 4th ed., Public Health Service, NIH, Washington DC, 1987]. A HindIII site and a BamHI site were introduced into the V region primer and the J region primer, respectively. PCR was conducted in accordance with the protocol of CETUS. That is, each 100 pmol of these primers were employed and reagents for PCR were those in a kit manufactured by CETUS. PCR was conducted by 25
 45 cycles, each cycle comprising 94°C for 1 minute, 55°C for 1 minute and 72°C for 1 minute. After PCR, the obtained DNA fragments were cloned into the HincII site of pUC18 (manufactured by Takara Shuzo; the reagents used in Examples were those manufactured by Takara Shuzo or Toyobo unless otherwise mentioned).

(3) Nucleotide sequence of anti-HIV antibody mouse V region gene

Using Sequenase Ver. 2 kit manufactured by Toyobo, the V region gene incorporated into pUC18 was sequenced. The nucleotide sequences of μ 39.1 and μ 5.5 obtained thereby are shown in Figs. 1 to 4. The amino acid sequences deduced from the nucleotide sequences are also shown in Figs. 1 to 4. Both
 55 nucleotide sequences of μ 39.1 and μ 5.5 exhibited rearrangement specific for the V region gene and showed an open reading frame (ORF) which allows for expression.

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(4) Preparation of anti-HIV chimeric antibody

In order to confirm that the V region genes μ 39.1 and μ 5.5 isolated in the above (2) are actually a gene coding for a V region responsible for an anti-HIV activity, a mouse-human chimeric antibody was prepared. For expression of a chimeric antibody, expression vectors HCMV-x and HCMV- γ 1 carrying enhancer and promoter of human cytomegalovirus (HCMV) [N. Whittle, et al., Protein Engineering, 1, 409 (1987)] were used, respectively. HCMV-x contains a human x chain constant region gene and HCMV- γ 1 contains a human γ 1 chain constant region gene. The μ 39.1 V region gene prepared in the above procedure (2) was digested with restriction enzymes HindIII and BamHI and the VH and VL fragments were incorporated into the HindIII-BamHI site of HCMV- γ 1 and HCMV-x, respectively. Figs. 5 and 6 show a structure of μ 39.1 chimeric antibody gene expression vectors (CH μ 39.1 and CL μ 39.1, respectively). Similarly, the μ 5.5 VH and VL region genes were incorporated into HCMV- γ 1 and HCMV-x (CH μ 5.5 and CL μ 5.5, respectively; cf. Figs. 5 and 6).

(5) Expression of anti-HIV chimeric antibody

An activity of an antibody shown by the μ 39.1 or μ 5.5 chimeric antibody gene constructed as mentioned above was examined in a transient expression system using COS7 cells [ATCC CRL 1651]. Using an Electroporation device manufactured by Bio-Rad, a mixture of CH μ 39.1 and CL μ 39.1 plasmid DNAs or a mixture of CH μ 5.5 and CL μ 5.5 plasmid DNAs were introduced into COS7 cells in accordance with the protocol of Bio-Rad and the cells were cultured in DMEM culture medium supplemented with 10% fetal calf serum (GIBCO). After three days, a culture supernatant was collected and an activity of antibodies present in the culture supernatant was measured by ELISA employing an anti-human IgG or SP-1 antigen peptide. As a result, as shown in Fig. 7, both expression products from a mixture of CH μ 39.1 and CL μ 39.1 plasmid DNAs and from a mixture of CH μ 5.5 and CL μ 5.5 plasmid DNAs bound to SP-1 peptide. Accordingly, it was confirmed that the μ 39.1 and μ 5.5 V region genes isolated in the procedure (2) are actually a gene coding for a V region of an antibody having an anti-HIV activity.

(6) Preparation of anti-HIV reshaped antibody

In order to study which portion of the VH or VL region of the cloned μ 39.1 or μ 5.5 is important for binding to an antigen, CDR (complementarity determining) regions of μ 39.1 and μ 5.5 were transplanted into human V regions. This was carried out in accordance with the method for preparing a reshaped antibody [Japanese Patent First Publication No. 62-296890]. CDR regions of VH region of μ 39.1 and μ 5.5 were transplanted into VH region having a framework (FR) region of human subgroup I [SGI: donated by Dr. Bendig in MRC Collaborative Center, England] (Figs. 8 and 10) whereas CDR regions of VL region of μ 39.1 and μ 5.5 were transplanted into VL region having a FR region of human x chain [REI: W. Palm and N. Hilschmann Z. Physiol. Chem., 356, 167 (1975)] (Figs. 9 and 11). Specifically, a reshaped antibody was prepared by an Amersham-PCR method which combines a kit from Amersham (Oligonucleotide-directed in vitro mutagenesis system version 2 code RPN. 1523) with PCR [Saiki, R. G. et al., Science, 239, 487 (1988)]. A long chain nucleotide coding for the portion to be transplanted of VH or VL region of μ 39.1 or μ 5.5 was annealed to M13 DNA in which the V region gene of SGI or REI was incorporated, and then an elongation and binding of DNA was conducted in a solution containing dCTP α S. The template M13 DNA was cleaved with NciI and the template DNA was digested with Exonuclease III to give only the mutated M13 DNA (up to this procedure was conducted in accordance with the protocol of Amersham). Then, using the product after Exonuclease III digestion as a template, PCR was carried out using a universal primer (UP: this primer contains a sequence complementary to the 5' site of M13mp18) and a reverse primer (RSP: this primer contains the same sequence as the 3' site of M13mp18). Each 20 pmol of these primers was employed and the reagents for PCR were those from CETUS. PCR was conducted by 25 cycles, each cycle comprising 94°C for 1 minute, 55°C for 1 minute and 74°C for 1 minute. After completion of PCR, the products were digested with BamHI/HindIII and the digested products were incorporated into the BamHI-HindIII site of pUC18, which was used for transformation of DH5 α (BRL). As a primary screening, a colony hybridization was conducted using the CDR primers employed in the mutagenesis in accordance with the protocol of the Amersham kit to select clones with successful mutagenesis in CDR. Then, as a secondary screening, a plasmid was prepared from the clones obtained in the primary screening and a sequencing was carried out with a Sequenase kit (Toyobo) to confirm a correct CDR transplanted. In this way, reshaped V regions of μ 39.1 or μ 5.5 (RH μ 39.1, RL μ 39.1, RH μ 5.5, RL μ 5.5, respectively; cf. Figs. 8 to 11) were obtained. As in the preparation of a chimeric antibody in the procedure (4), these reshaped V

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region fragments were digested with HindIII and BamHI restriction enzymes and the VH and VL fragments were incorporated into the HindIII-BamHI site of HCMV- γ 1 or HCMV- α , respectively. Thus, there were prepared μ 39.1 reshaped antibody gene expression vectors (RH μ 39.1 and RL μ 39.1, respectively) and μ 5.5 reshaped antibody gene expression vectors (RH μ 5.5 and RL μ 5.5, respectively).

5
(7) Expression of anti-HIV reshaped antibody

10 An activity of antibodies obtained by these reshaped μ 39.1 and μ 5.5 antibody genes was examined in the above-mentioned transient expression system using COS7 cells. As in the procedure (5), a culture supernatant of the cells where the gene was incorporated was collected and an activity of antibodies present in the culture supernatant was measured by ELISA employing an anti-human IgG or SP-1 peptide. As a result, as shown in Fig. 7, both expression products from a mixture of RH μ 39.1 and RL μ 39.1 plasmid DNAs and from a mixture of RH μ 5.5 and RL μ 5.5 plasmid DNAs bound to SP-1 peptide. Accordingly, it was confirmed that, in the amino acid sequences of μ 39.1 and μ 5.5 as shown in Figs. 9 to 12, the transplanted
15 CDR regions were the most important region for exerting an anti-HIV activity. From this result, it was confirmed that the genes coding for these regions are a quite useful gene for preparing a recombinant anti-HIV antibody.

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Sequence Listing

6 SEQ ID NO: 1
SEQUENCE LENGTH: 357
SEQUENCE TYPE: nucleic acid
10 STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
15 FEATURE
ORIGINAL SOURCE
ORGANISM: mouse
20 SEQUENCE
CAG ATC CAG ATG GTG CAG TCT GGA CCT GAG TTG AAG AAG CCT GGA GAG 48
Gln Ile Gln Met Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
25 1 5 10 15
ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ACC TTC ACA AAA TAT 96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
30 20 25 30
GGA ATG AAC TGG GTG AAA CAG ACT CCA GGA AAG GGT TTA AAG TGG ATG 144
Gly Met Asn Trp Val Lys Gln Thr Pro Gly Lys Gly Leu Lys Trp Met
35 35 40 45
GGC TGG AAA AAC ACC AAT ACT GGA GAG TCA ACA CAT GTT GAA GAG TTC 192
40 Gly Trp Lys Asn Thr Asn Thr Gly Glu Ser Thr His Val Glu Glu Phe
50 55 60

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AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC AGT ACT GCC TAT 240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80
5 TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC ACG GCT ACA TAT TTC TGT 288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
10 85 90 95
GCA AGA GAA TAT GAT TAC GAC GGG GGC TTT TCT TAC TGG GGC CAA GGG 336
Ala Arg Glu Tyr Asp Tyr Asp Gly Gly Phe Ser Tyr Trp Gly Gln Gly
15 100 105 110
ACT CTG GTC ACT GTC TCT GCA 357
Thr Leu Val Thr Val Ser Ala
20 115

SEQ ID NO: 2

25 SEQUENCE LENGTH: 321

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

30 TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

FEATURE

35 ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE

40 GAC ATT GTG ATG ACC CAG TCT CAC AAA TTC ATG TCC ACA TCA GTA GGA 48
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
45 1 5 10 15

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GAC AGG GTC AGC ATC ACC TGC AAG GCC AGT CAG GAT GTG GGT GCT GAT 96
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Ala Asp
5 20 25 30
GTA GCC TGG TAT CAA CAG AAA CCA GGA CAA TCT CCT AAA CAA CTG ATT 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Gln Leu Ile
10 35 40 45
TCC TGG GCA TCC ACC CGG CAC ACT GGA GTC CCT GAT CGC TTC ACA GGC 192
Ser Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
15 50 55 60
AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATT ACC AAT GTG CAG TCT 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
20 65 70 75 80
GAA GAC TTG GCA GAT TAT TTC TGT CAG CAA TAT AGC AGC TTT CCT CTC 288
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Phe Pro Leu
25 85 90 95
ACG TTC GGT ACT GGG ACC AAG TTG GAG CTG AGA 321
Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Arg
30 100 105

SEQ ID NO: 3
35 SEQUENCE LENGTH: 354
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: double
40 TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
45 FEATURE
50
55

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ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE

5 GAG GTC CAG CTG CAA CAG TCT GGG CCT GAC CTG GTG AAG CCT GGG GCT 48
 Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala
 10 1 5 10 15
 TCA GTG AAG ATA TCC TGC AAG ACT TCT GGA TAC ACA TTC ACT GAA TAC 96
 Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 15 20 25 30
 ACC ATG CAC TGG GTG AAG CAG AGC CAT GGA AGG AGC CTT GAG TGG ATT 144
 Thr Met His Trp Val Lys Gln Ser His Gly Arg Ser Leu Glu Trp Ile
 20 35 40 45
 GGA GGT ATT AAT CCT AAC AAT GGT GAT ACT AGC TAC ACC CAG AAG TTC 192
 Gly Gly Ile Asn Pro Asn Asn Gly Asp Thr Ser Tyr Thr Gln Lys Phe
 25 50 55 60
 AAG GGC AAG GCC ACA TTG ACT GTA GAC AAG TCC TCC AGC ACA GCC TAC 240
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 30 65 70 75 80
 ATG GAG CTC CGC AGC CTG ACA TCT GAG GAT TCT GCA GTC TAT TAC TGT 288
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 35 85 90 95
 GCA ACA CCC TAC TAT GCC TAT GCT ATT GAC TCC TGG GGT CAA GGA ACC 336
 40 Ala Thr Pro Tyr Tyr Ala Tyr Ala Ile Asp Ser Trp Gly Gln Gly Thr
 100 105 110

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TCA GTC ACC GTC TCC TCA

354

Ser Val Thr Val Ser Ser

5 115

SEQ ID NO: 4

10 SEQUENCE LENGTH: 333

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

FEATURE

20 ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE

25 GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT GTG TCT CTA GGG 48

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly

30 1 5 10 15

CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT 96

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp

35 20 25 30

GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA GGA CAG CCA CCC 144

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro

40 35 40 45

AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT GGG ATC CCA GCC 192

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala

45 50 55 60

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AGC TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC AAC ATC CAT 240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
5 65 70 75 80
CCT GTG GAG CAG GAG GAT GGT GCA ACC TAT TAC TGT CAG CAA AGT AAT 288
Pro Val Glu Glu Glu Asp Gly Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
10 85 90 95
GAG GAT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA 333
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
15 100 105 110

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SEQ ID NO: 5

20 SEQUENCE LENGTH: 357

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

25 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic nucleic acid)

FEATURE

30 ORIGINAL SOURCE

ORGANISM: mouse and human

SEQUENCE

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35 CAG GTG CAA CTA GTG CAG TCC GGC GCC GAA GTG AAG AAA CCC GGT GCT 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
40 TCC GTG AAG GTG AGC TGT AAA GCT AGC GGT TAT ACC TTC ACA AAA TAT 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
20 25 30
45

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GGA ATG AAC TGG GTT AGA CAG GCC CCA GGC CAA GGG CTC AAG TGG ATG 144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
5 35 40 45
GGC TGG AAA AAC ACC AAT ACT GGA GAG TCA ACA CAT GTT GAG GAG TTT 192
Gly Trp Lys Asn Thr Asn Thr Gly Glu Ser Thr His Val Glu Glu Phe
10 50 55 60
AAG GGC AGG GTT ACC ATG TCC TTG GAC ACC TCT ACA AAC ACC GCC TAC 240
Lys Gly Arg Val Thr Met Ser Leu Asp Thr Ser Thr Asn Thr Ala Tyr
15 65 70 75 80
ATG GAA CTG TCC AGC CTG CGC TCC GAG GAC ACT GCA GTT TAC TAC TGC 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
20 85 90 95
GCC AGA GAA TAT GAT TAC GAC GGC GGC TTC TCC TAT TGG GGA CAG GGT 336
Ala Arg Glu Tyr Asp Tyr Asp Gly Gly Phe Ser Tyr Trp Gly Gln Gly
25 100 105 110
ACC CTT GTC ACC GTC AGT TCA 357
Thr Leu Val Thr Val Ser Ser
30 115

SEQ ID NO: 6
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SEQUENCE LENGTH: 321
SEQUENCE TYPE: nucleic acid
40
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic nucleic acid)
45
FEATURE
50
55

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ORIGINAL SOURCE

ORGANISM: mouse and human

5 SEQUENCE

GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
70 1 5 10 15
GAC AGA GTG ACC ATC ACC TGT AAA GCC AGC CAG GAT GTG GGT GCT GAT 96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Ala Asp
15 20 25 30
GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC 144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
20 35 40 45
TCC TGG GCA TCC ACC CGG CAC ACT GGT GTG CCA AGC AGA TTC AGC GGT 192
Ser Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
25 50 55 60
AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA 240
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
30 65 70 75 80
GAG GAC ATC GCC ACA TAC TAC TGC CAA CAA TAT AGC AGC TTT CCA CTC 288
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Phe Pro Leu
35 85 90 95
ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 321
40 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

45 SEQ ID NO: 7

50

55

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SEQUENCE LENGTH: 354
SEQUENCE TYPE: nucleic acid
5 STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic nucleic acid)
70 FEATURE
ORIGINAL SOURCE
ORGANISM: mouse and human
16 SEQUENCE
CAG GTG CAA CTA GTG CAG TCC GGC GCC GAA GTG AAG AAA CCC GGT GCT 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
20 1 5 10 15
TCC GTG AAG GTG AGC TGT AAA GCT AGC GGT TAT ACC TTC ACT GAA TAC 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
25 20 25 30
ACC ATG CAT TGG GTT AGA CAG GCC CCA GGC CAA GGG CTC GAG TGG ATT 144
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
30 35 40 45
GGC GGT ATT AAC CCT AAC AAT GGC GAT ACA AGC TAT ACC CAG AAG TTT 192
Gly Gly Ile Asn Pro Asn Asn Gly Asp Thr Ser Tyr Thr Gln Lys Phe
35 50 55 60
AAG GGC AAG GCT ACC ATG ACC GTA GAC ACC TCT ACA AAC ACC GCC TAC 240
40 Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

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ATG GAA CTG TCC AGC CTG CGC TCC GAG GAC ACT GCA GTT TAC TAC TGC 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
5 85 90 95
GCC ACA CCC TAC TAC GCC TAC GCT ATT GAC TCC TGG GGA CAG GGT ACC 336
Ala Thr Pro Tyr Tyr Ala Tyr Ala Ile Asp Ser Trp Gly Gln Gly Thr
10 100 105 110
CTT GTC ACC GTC AGT TCA 354
Leu Val Thr Val Ser Ser
15 115

SEQ ID NO: 8
20 SEQUENCE LENGTH: 333
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: double
25 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid (synthetic nucleic acid)
FEATURE
30 ORIGINAL SOURCE
ORGANISM: mouse and human

SEQUENCE
35 GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
40 GAC AGA GTG ACC ATC ACC TGT AAG GCC AGC CAA AGT GTT GAT TAT GAT 96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
45 20 25 30

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GGT GAT AGT TAT ATG AAC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA 144
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45
 AAG CTG CTG ATC TAC GCT GCA TCC AAT CTA GAA TCT GGT GTG CCA AGC 192
 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
 50 55 60
 AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC 240
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
 65 70 75 80
 AGC CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA AGT AAT 288
 Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
 85 90 95
 GAG GAC CCA TGG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 333
 Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Claims

1. A genetic recombinant anti-HIV antibody H chain comprising an amino acid sequence derived from a mouse antibody and an amino acid sequence derived from a human antibody characterized by that complementarity determining regions (CDR1 to CDR3) have the following amino acid sequences, said recombinant anti-HIV antibody H chain having a neutralizing activity against human immunodeficiency virus (HIV):
- CDR1: Lys-Tyr-Gly-Met-Asn
 CDR2: Trp-Lys-Asn-Thr-Asn-Thr-Gly-Glu-Ser-Thr-His-Val-Glu-Glu-Phe-Lys-Gly
 CDR3: Glu-Tyr-Asp-Tyr-Asp-Gly-Gly-Phe-Ser-Tyr.
2. The recombinant anti-HIV antibody H chain of claim 1 wherein one amino acid at the C terminus of FR1 adjacent to the complementarity determining region CDR1 in a variable region is threonine (Thr), a four amino acid sequence at the C terminus of FR2 adjacent to CDR2 is Lys-Trp-Met-Gly, a five amino acid sequence at the N terminus of FR3 adjacent to CDR2 is Arg-Val-Thr-Met-Ser, and one amino acid at the C terminus of FR3 adjacent to CDR3 is arginine (Arg).
3. The recombinant anti-HIV antibody H chain of claim 1 wherein said recombinant anti-HIV antibody H chain is a reshaped antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 119 in Sequence Listing: SEQ ID NO: 5.
4. The recombinant anti-HIV antibody H chain of claim 1 wherein said recombinant anti-HIV antibody H chain is a chimeric antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 119 in Sequence Listing: SEQ ID NO: 1.
5. A genetic recombinant anti-HIV antibody L chain comprising an amino acid sequence derived from a mouse antibody and an amino acid sequence derived from a human antibody characterized by that complementarity determining regions (CDR1 to CDR3) have the following amino acid sequences, said recombinant anti-HIV antibody L chain having a neutralizing activity against human immunodeficiency virus (HIV):

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CDR1: Lys-Ala-Ser-Gln-Asp-Val-Gly-Ala-Asp-Val-Ala

CDR2: Trp-Ala-Ser-Thr-Arg-His-Thr

CDR3: Gln-Gln-Tyr-Ser-Ser-Phe-Pro-Leu-Thr.

- 5 6. The recombinant anti-HIV antibody L chain of claim 5 wherein said recombinant anti-HIV antibody L chain is a reshaped antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 107 in Sequence Listing: SEQ ID NO: 6.
- 10 7. The recombinant anti-HIV antibody L chain of claim 5 wherein said recombinant anti-HIV antibody L chain is a chimeric antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 107 in Sequence Listing: SEQ ID NO: 2.
8. A recombinant anti-HIV antibody comprising the recombinant anti-HIV antibody H chain of claim 1 and the anti-HIV antibody L chain of claim 5.
- 15 9. A genetic recombinant anti-HIV antibody H chain comprising an amino acid sequence derived from a mouse antibody and an amino acid sequence derived from a human antibody characterized by that complementarity determining regions (CDR1 to CDR3) have the following amino acid sequences, said recombinant anti-HIV antibody H chain having a neutralizing activity against human immunodeficiency virus (HIV):
- 20 CDR1: Glu-Tyr-Thr-Met-His
CDR2: Gly-Ile-Asn-Pro-Asn-Asn-Gly-Asp-Thr-Ser-Tyr-Thr-Gln-Lys-Phe-Lys-Gly
CDR3: Pro-Tyr-Tyr-Ala-Tyr-Ala-Ile-Asp-Ser.
- 25 10. The recombinant anti-HIV antibody H chain of claim 9 wherein one amino acid at the C terminus of FR1 adjacent to the complementarity determining region CDR1 in a variable region is threonine (Thr), a two amino acid sequence at the C terminus of FR2 adjacent to CDR2 is Ile-Gly, a six amino acid sequence at the N terminus of FR3 adjacent to CDR2 is Lys-Ala-Thr-Met-Thr-Val, and one amino acid at the C terminus of FR3 adjacent to CDR3 is threonine (Thr).
- 30 11. The recombinant anti-HIV antibody H chain of claim 9 wherein said recombinant anti-HIV antibody H chain is a reshaped antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 118 in Sequence Listing: SEQ ID NO: 7.
- 35 12. The recombinant anti-HIV antibody H chain of claim 9 wherein said recombinant anti-HIV antibody H chain is a chimeric antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 118 in Sequence Listing: SEQ ID NO: 3.
- 40 13. A genetic recombinant anti-HIV antibody L chain comprising an amino acid sequence derived from a mouse antibody and an amino acid sequence derived from a human antibody characterized by that complementarity determining regions (CDR1 to CDR3) have the following amino acid sequences, said recombinant anti-HIV antibody H chain having a neutralizing activity against human immunodeficiency virus (HIV):
- 45 CDR1: Lys-Ala-Ser-Gln-Ser-Val-Asp-Tyr-Asp-Gly-Asp-Ser-Tyr-Met-Asn
CDR2: Ala-Ala-Ser-Asn-Leu-Glu-Ser
CDR3: Gln-Gln-Ser-Asn-Glu-Asp-Pro-Trp-Thr.
- 50 14. The recombinant anti-HIV antibody L chain of claim 13 wherein said recombinant anti-HIV antibody L chain is a reshaped antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 111 in Sequence Listing: SEQ ID NO: 8.
- 55 15. The recombinant anti-HIV antibody L chain of claim 13 wherein said recombinant anti-HIV antibody L chain is a chimeric antibody, and a whole amino acid sequence of a variable region is an amino acid sequence of amino acid Nos. 1 to 111 in sequence Listing: SEQ ID NO: 4.
16. A recombinant anti-HIV antibody comprising the recombinant anti-HIV antibody H chain of claim 9 and the anti-HIV antibody L chain of claim 13.

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17. A DNA fragment coding for an H chain variable region, or a portion thereof, of an antibody having a neutralizing activity against human immunodeficiency virus (HIV), said DNA fragment having a nucleotide sequence of nucleotide Nos. 1 to 357 in Sequence Listing: SEQ ID NO: 1 or a portion of said nucleotide sequence.
18. A DNA fragment coding for an L chain variable region, or a portion thereof, of an antibody having a neutralizing activity against human immunodeficiency virus (HIV), said DNA fragment having a nucleotide sequence of nucleotide Nos. 1 to 321 in Sequence Listing: SEQ ID NO: 2 or a portion of said nucleotide sequence.
19. A DNA fragment coding for an H chain variable region, or a portion thereof, of an antibody having a neutralizing activity against human immunodeficiency virus (HIV), said DNA fragment having a nucleotide sequence of nucleotide Nos. 1 to 354 in Sequence Listing: SEQ ID NO: 3 or a portion of said nucleotide sequence.
20. A DNA fragment coding for an L chain variable region, or a portion thereof, of an antibody having a neutralizing activity against human immunodeficiency virus (HIV), said DNA fragment having a nucleotide sequence of nucleotide Nos. 1 to 333 in Sequence Listing: SEQ ID NO: 4 or a portion of said nucleotide sequence.
21. A process for preparing a recombinant anti-HIV antibody which comprises constructing an expression vector by using the DNA fragment of claim 17 and the DNA fragment of claim 18 and a DNA fragment coding for a human immunoglobulin, said expression vector allowing for expression of a recombinant antibody wherein at least complementarity determining regions have an amino acid sequence derived from a mouse antibody, expressing the recombinant DNA in an animal cell, and collecting said antibody.
22. A process for preparing a recombinant anti-HIV antibody which comprises constructing an expression vector by using the DNA fragment of claim 19 and the DNA fragment of claim 20 and a DNA fragment coding for a human immunoglobulin, said expression vector allowing for expression of a recombinant antibody wherein at least complementarity determining regions have an amino acid sequence derived from a mouse antibody, expressing the recombinant DNA in an animal cell, and collecting said antibody.

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Fig. 1

| FR1
1 CAGATCCAGATGGTGCAGTCTGGACCTGAGTTGAAGAAGCCTGGAGAGACAGTCAAGATC
GlnIleGlnMetValGlnSerGlyProGluLeuLysLysProGlyGluThrValLysIle

| CDR1 | FR2
61 TCCTGCAAGGCTTCTGGGTATACCTTCACAAAATATGGAATGAACTGGGTGAAACAGACT
SerCysLysAlaSerGlyTyrThrPheThrLysTyrGlyMetAsnTrpValLysGlnThr

| CDR2
121 CCAGCAAAGGCTTTAAAGTGGATGGGCTGGAAAAACACCAATACTGGAGAGTCAACACAT
ProGlyLysGlyLeuLysTrpMetGlyTrpLysAsnThrAsnThrGlyGluSerThrHis

| FR3
181 GTTGAAGAGTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGTACTGCCTAT
ValGluGluPheLysGlyArgPheAlaPheSerLeuGluThrSerAlaSerThrAlaTyr

|
241 TTGCAGATCAACAACCTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGAGAATAT
LeuGlnIleAsnAsnLeuLysAsnGluAspThrAlaThrTyrPheCysAlaArgGluTyr

CDR3 | FR4
301 GATTACGACGGGGGCTTTTCTTACTGGGGCCAAGGGA CTCTGGTCACTGTCTCTGCA
AspTyrAspGlyGlyPheSerTyrTrpGlyGlnGlyThrLeuValThrValSerAla

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Fig. 2

| FRI
1 GACATTGTGATGACCCAGTCTCACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGC
AspIleValMetThrGlnSerHisLysPheMetSerThrSerValGlyAspArgValSer

| CDR1 | FR2
61 ATCACCTGCAAGGCCAGTCAGGATGTGGGTGCTGATGTAGCCTGCTATCAACAGAAACCA
IleThrCysLysAlaSerGlnAspValGlyAlaAspValAlaTrpTyrGlnGlnLysPro

| CDR2 | FR3
121 GGACAATCTCCTAAACAACCTGATTTCTGGGCATCCACCCGGCACACTGGAGTCCCTGAT
GlyGlnSerProLysGlnLeuIleSerTrpAlaSerThrArgHisThrGlyValProAsp

181 CGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTACCAATGTGCAGTCT
ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleThrAsnValGlnSer

| CDR3 | FR4
241 GAAGACTTGGCAGATTATTTCTGTCAGCAATATAGCAGCTTTCCTCTCAGTTTCGGTACT
GluAspLeuAlaAspTyrPheCysGlnGlnTyrSerSerPheProLeuThrPheGlyThr

301 GGGACCAAGTTGGAGCTGAGA
GlyThrLysLeuGluLeuArg

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Fig. 3

| FR1
1 GAGGTCCAGCTGCAACAGTCTGGGCCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA
GluValGlnLeuGlnGlnSerGlyProAspLeuValLysProGlyAlaSerValLysIle

| CDR1 | FR2
61 TCCTGCAAGACTTCTGGATACACATTCAGTGAATACACCATGCACTGGGTGAAGCAGAGC
SerCysLysThrSerGlyTyrThrPheThrGluTyrThrMetHisTrpValLysGlnSer

| CDR2
121 CATGGAAGGAGCCTTGAGTGGATTGGAGGTATTAATCCTAACAATGGTGATACTAGCTAC
HisGlyArgSerLeuGluTrpIleGlyGlyIleAsnProAsnAsnGlyAspThrSerTyr

| FR3
181 ACCCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC
ThrGlnLysPheLysGlyLysAlaThrLeuThrValAspLysSerSerSerThrAlaTyr

|
241 ATGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAACACCCTAC
MetGluLeuArgSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaThrProTyr

CDR3 | FR4
301 TATGCCTATGCTATTGACTCCTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
TyrAlaTyrAlaIleAspSerTrpGlyGlnGlyThrSerValThrValSerSer

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Fig. 4

| FR1
1 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
AspIleValLeuThrGlnSerProAlaSerLeuAlaValSerLeuGlyGlnArgAlaThr

| CDR1 | FR2
61 ATCTCCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAACTGGTAC
IleSerCysLysAlaSerGlnSerValAspTyrAspGlyAspSerTyrMetAsnTrpTyr

| CDR2
121 CAACAGAAACCAGGACAGCCACCCAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
GlnGlnLysProGlyGlnProProLysLeuLeuIleTyrAlaAlaSerAsnLeuGluSer

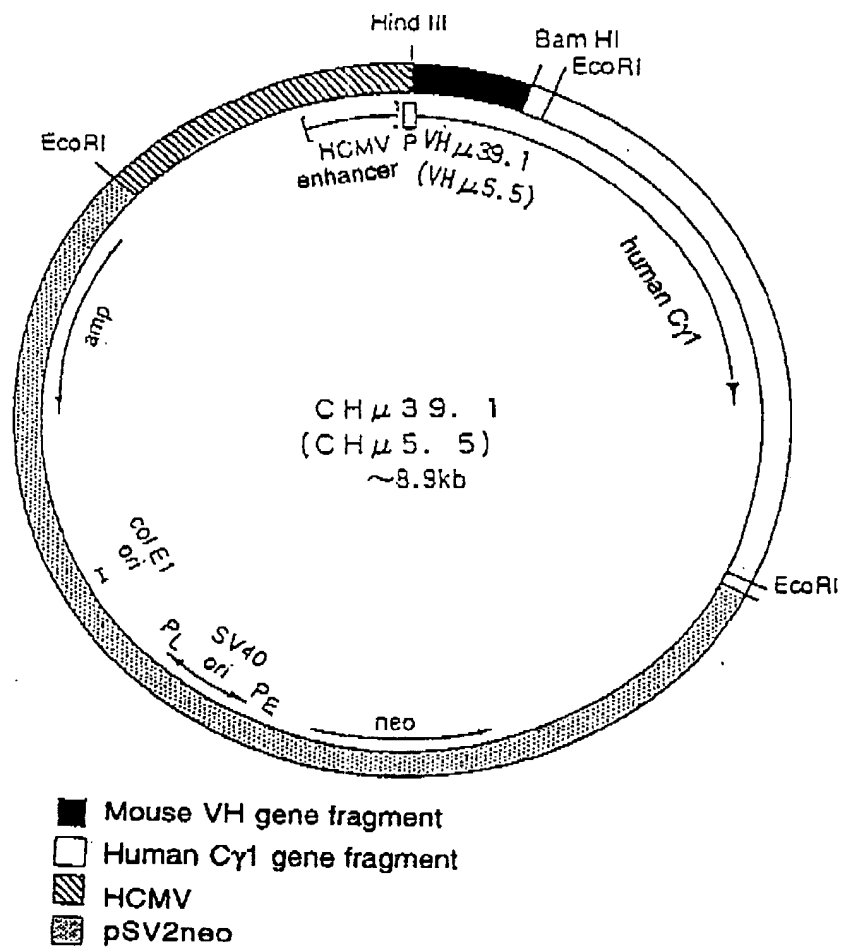
| FR3
181 GGGATCCCAGCCAGGTTTAGTGCCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
GlyIleProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuAsnIleHis

| CDR3
241 CCTGTGGAGGAGGAGGATGGTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCGTGG
ProValGluGluGluAspGlyAlaThrTyrTyrCysGlnGlnSerAsnGluAspProTrp

| FR4
301 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA
ThrPheGlyGlyGlyThrLysLeuGluIleLys

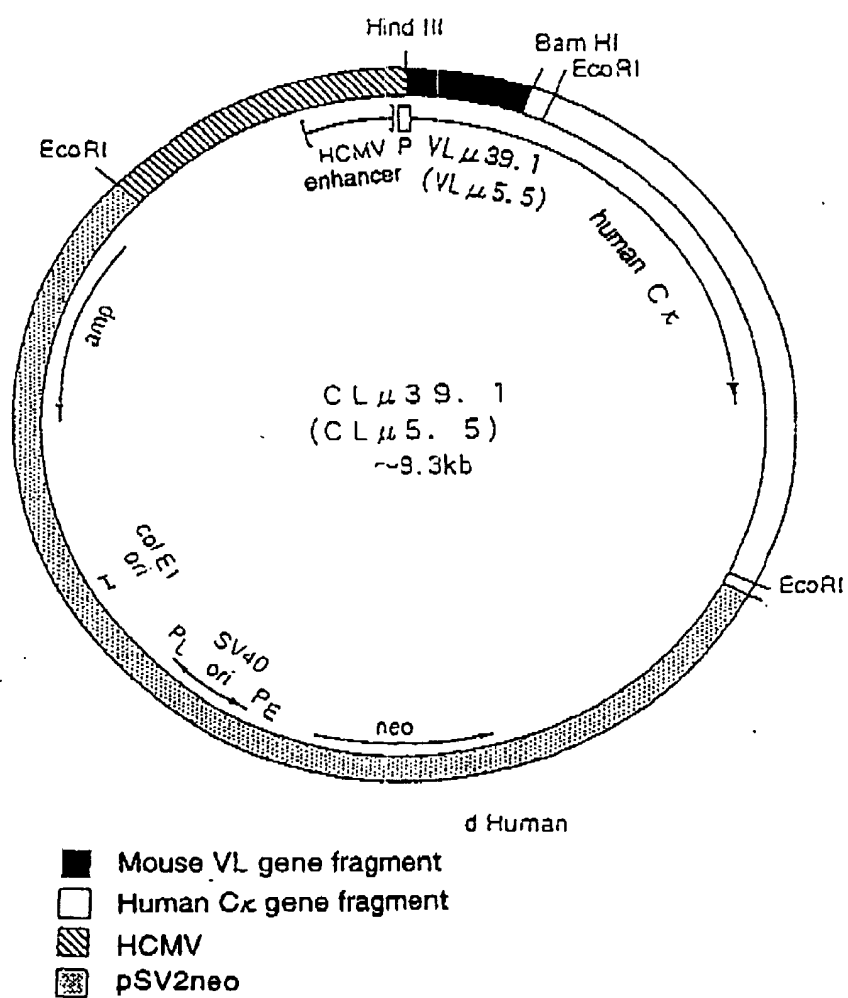
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Fig. 5



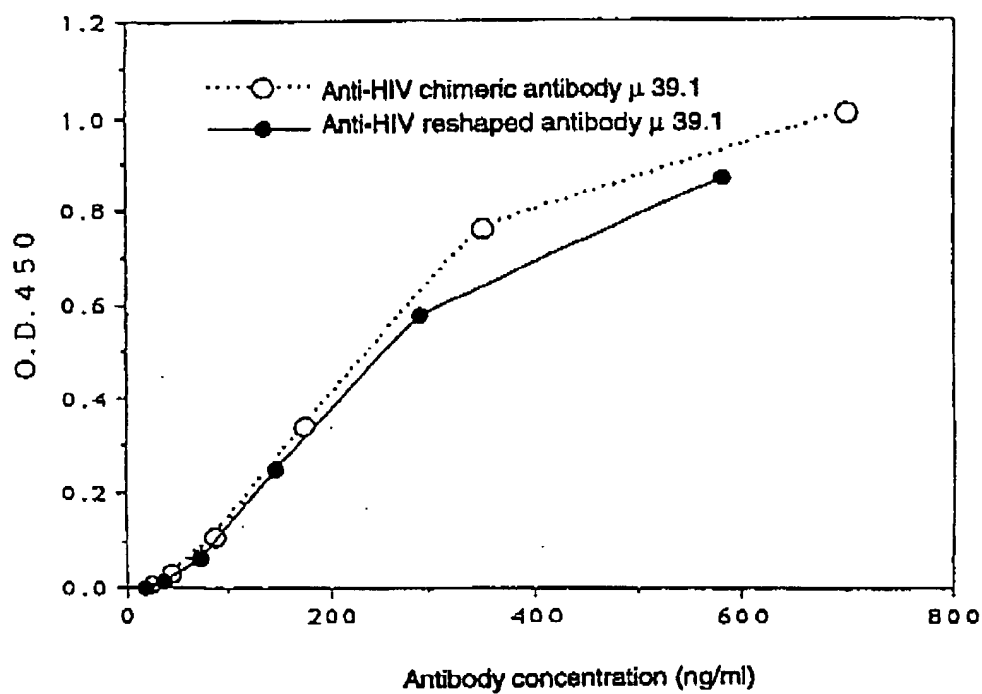
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Fig. 6



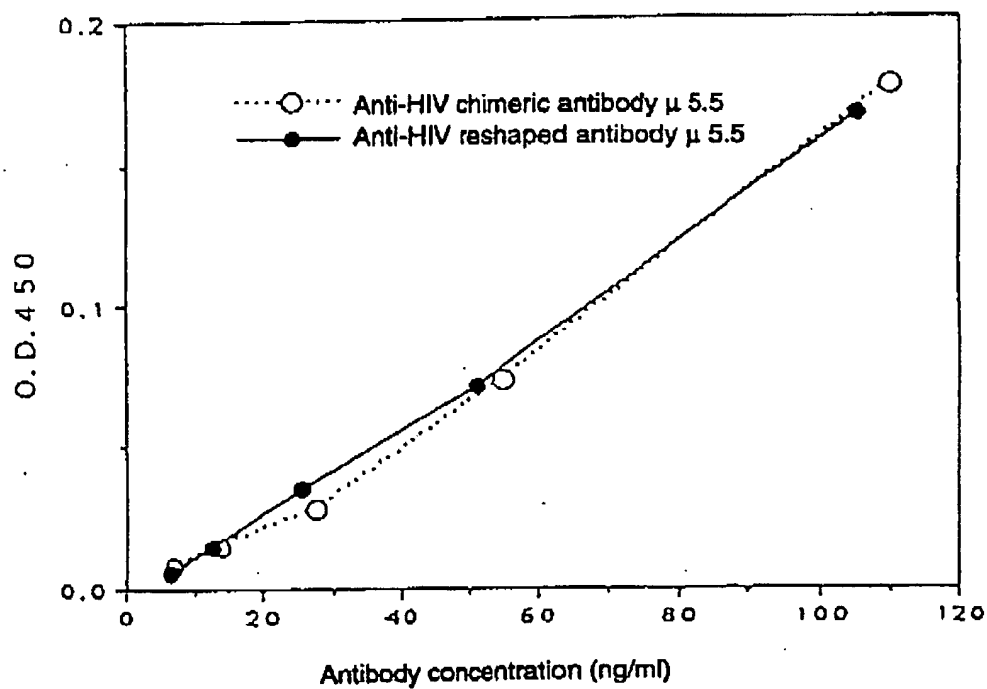
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Fig. 7



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Fig. 8



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Fig. 9

| FR1
1 CAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAGAAACCCGGTGCTTCCGTGAAGCTG
GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSerValLysVal

| CDR1 | FR2
61 AGCTGTAAAGCTAGCGGTTATACCTTCACAAAATATGGAATGAACTGGGTTAGACAGGCC
SerCysLysAlaSerGlyTyrThrPheThrLysTyrGlyMetAsnTrpValArgGlnAla

| CDR2
121 CCAGGCCAAGGGCTCAAGTGGATGGGCTGGAAAAACACCAATACTGGAGAGTCAACACAT
ProGlyGlnGlyLeuLysTrpMetGlyTrpLysAsnThrAsnThrGlyGluSerThrHis

| FR3
181 GTTGAAGAGTTTAAGGGCAGGGTTACCATGTCCTTGGACACCTCTACAAACACCGCCTAC
ValGluGluPheLysGlyArgValThrMetSerLeuAspThrSerThrAsnThrAlaTyr

|
241 ATGGAAGTGTCCAGCCTGCCCTCCGAGGACACTGCAGTTTACTACTGCGCCAGAGAATAT
MetGluLeuSerSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgGluTyr

CDR3 | FR4
301 GATTACGACGGGGGCTTCTCCTATTGGGGACAGGGTACCCTTGTACCGTCAGTTCA
AspTyrAspGlyGlyPheSerTyrTrpGlyGlnGlyThrLeuValThrValSerSer

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Fig. 10

| FR1
1 GACATCCAGATGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACAGACTGACC
AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr

| CDR1 | FR2
61 ATCACCTGTAAAGCCAGCCAGGATGTGGGTGCTGATGTAGCTTGGTACCAGCAGAAAGCCA
IleThrCysLysAlaSerGlnAspValGlyAlaAspValAlaTrpTyrGlnGlnLysPro

| CDR2 | FR3
121 GGTAAGGCTCCAAAGCTGCTGATCTCCTGGGCATCCACCCGGCACACTGGTGTGCCAAGC
GlyLysAlaProLysLeuLeuIleSerTrpAlaSerThrArgHisThrGlyValProSer

181 AGATTACGGGTAGCGGTAGCGGTACCGACTTCACCTTACCATCAGCAGCCTCCAGCCA
ArgPheSerGlySerGlySerGlyThrAspPheThrPheThrIleSerSerLeuGlnPro

| CDR3 | FR4
241 GAGGACATCGCCACATACTACTGCCAACAAATATAGCAGCTTTCCACTCACGTTTCGGCCAA
GluAspIleAlaThrTyrTyrCysGlnGlnTyrSerSerPheProLeuThrPheGlyGln

301 GGGACCAAGGTGGAAATCAAA
GlyThrLysValGluIleLys

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Fig. 11

| FR1
1 CAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAGAAACCCGGTGGCTTCCGTGAAGGTG
GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSerValLysVal

| CDR1 | FR2
61 AGCTGTAAAGCTAGCGGTTATACCTTCACTGAATACACCATGCATTGGGTTAGACAGGCC
SerCysLysAlaSerGlyTyrThrPheThrGluTyrThrMetHisTrpValArgGlnAla

| CDR2
121 CCAGGCCAAGGGCTCGAGTGGATTGGCGGTATTAACCCTAACAATGGCGATACAAGCTAT
ProGlyGlnGlyLeuGluTrpIleGlyGlyIleAsnProAsnAsnGlyAspThrSerTyr

| FR3
181. ACCCAGAAGTTTAAGGGCAAGGCTACCATGACCGTAGACACCTCTACAAACACCGCCTAC
ThrGlnLysPheLysGlyLysAlaThrMetThrValAspThrSerThrAsnThrAlaTyr

|
241 ATGGAAGTGTCCAGCCTGCGCTCCGAGGACACTGCAGTTTACTACTGCGCCACACCGCTAC
MetGluLeuSerSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaThrProTyr

CDR3 | FR4
301 TACGCCTACGCTATTGACTCCTGGCGACAGGCTACCCCTTGTCACCGTCAGTTCA
TyrAlaTyrAlaIleAspSerTrpGlyGlnGlyThrLeuValThrValSerSer

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Fig. 12

| FR1
1 GACATCCAGATGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACAGAGTGACC
AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr

| CDR1 | FR2
61 ATCACCTGTAAGGCCAGCCAAAGTGTTGATTATGATGGIGATAGTTATATGAACTGGTAC
IleThrCysLysAlaSerGlnSerValAspTyrAspGlyAspSerTyrMetAsnTrpTyr

| CDR2
121 CAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACGCTGCATCCAATCTAGAATCT
GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerAsnLeuGluSer

| FR3
181 GGTGTGCCAAGCAGATTACCGGTAGCGGTAGCGGTACCGACTTACCTTCACCATCAGC
GlyValProSerArgPheSerGlySerGlySerGlyThrAspPheThrPheThrIleSer

| CDR3
241 AGCCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCAAAGTAATGAGGACCCATGG
SerLeuGlnProGluAspIleAlaThrTyrTyrCysGlnGlnSerAsnGluAspProTrp

| FR4
301 ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
ThrPheGlyGlnGlyThrLysValGluIleLys

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP93/00039

A. CLASSIFICATION OF SUBJECT MATTER Int. Cl ⁵ C07K15/28, C12P21/08, C12N15/13// A61K39/395 (C12P21/08, C12R1:91) According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int. Cl ⁵ C07K15/28, C12P21/08, C12N15/13 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) CAS ONLINE, BIOSIS PREVIEWS		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JP, A, 4-152893 (Juridical Foundation The Chemo-Sero-Therapeutic Research Institute) May 26, 1992 (26. 05. 92), & EP, A1, 465979 & AU, A, 9180107 & CA, A, 2046016	1-22
Y	JP, A, 62-296890 (Gregory Poll Winter), December 24, 1987 (24. 12. 87), & EP, A2, 239400 & GB, A, 2188638	1-22
Y	The Journal of Biological Chemistry, Vol. 266, No. 22, (1991), R. Attanasio et al., "Structural Characterization of a Cross-reactive Idiotypic Shared by Monoclonal Antibodies Specific for the Human CD4 Molecule" p. 14611-14619	1-22
A	JP, A, 2-2352 (Juridical Foundation The Chemo-Sero-Therapeutic Research Institute) January 8, 1990 (08. 01. 90),	1-22
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Date of the actual completion of the international search April 12, 1993 (12. 04. 93)		Date of mailing of the international search report April 27, 1993 (27. 04. 93)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP93/00039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	& EP, A2, 327000 & AU, A, 8928954	

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